

OM protein - protein search, using sw model

Run on: December 20, 2004, 14:44:03 ; Search time 17.2857 Seconds
(without alignments)
84.405 Million cell updates/sec

Title: US-10-797-748-4

Perfect score: 147
Sequence: 1 MDCKDECTCAPDCXKADCKC 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	147	100.0	22	4 US-09-948-495A-4	Sequence 4, Appl
2	147	100.0	48	4 US-09-948-495A-2	Sequence 2, Appl
3	73.5	50.0	61	4 US-09-919-039-31	Sequence 31, Appl
4	73.5	50.0	254	2 US-08-767-026-7	Sequence 7, Appl
5	73.5	50.0	254	4 US-09-319-275A-7	Sequence 7, Appl
6	70.5	48.0	61	2 US-08-785-530-5	Sequence 5, Appl
7	70.5	48.0	61	2 US-09-123-850-5	Sequence 5, Appl
8	70	47.6	61	2 US-08-785-530-4	Sequence 4, Appl
9	70	47.6	61	2 US-08-785-530-6	Sequence 4, Appl
10	70	47.6	61	2 US-09-123-850-4	Sequence 4, Appl
11	70	47.6	61	2 US-09-123-850-6	Sequence 6, Appl

ALIGNMENTS

12	70	47.6	62	3 US-07-780-717C-5	Sequence 5, Appl
13	69	46.9	68	1 US-07-696-051B-1	Sequence 1, Appl
14	69	46.9	68	1 US-07-924-063A-1	Sequence 1, Appl
15	69	46.9	68	1 US-08-138-340B-2	Sequence 2, Appl
16	68.5	46.6	61	4 US-09-919-039-272	Sequence 272, App
17	64.5	43.9	14	1 US-08-322-962-12	Sequence 12, Appl
18	64.5	43.9	14	3 US-08-450-653-12	Sequence 12, Appl
19	64.5	43.9	61	2 US-08-785-530-3	Sequence 3, Appl
20	64.5	43.9	61	2 US-09-123-850-3	Sequence 3, Appl
21	64.5	43.9	61	4 US-09-919-039-195	Sequence 155, App
22	64.5	43.9	1345	2 US-08-977-767-3	Sequence 3, Appl
23	64.5	43.9	2732	4 US-09-086-436-30	Sequence 30, Appl
24	63	42.9	2088	4 US-09-548-372D-13	Sequence 13, Appl
25	63	42.9	2088	4 US-09-548-367D-13	Sequence 13, Appl
26	63	42.9	2088	4 US-09-551-853D-13	Sequence 13, Appl
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30	62.5	42.5	61	4 US-09-919-039-245	Sequence 245, App
31	62	42.2	38	2 US-08-902-516-47	Sequence 47, Appl
32	62	42.2	38	4 US-09-847-185-47	Sequence 47823, A
33	61.5	41.8	82	4 US-09-270-767-47823	Sequence 32606, A
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35	61.5	41.8	1400	3 US-08-630-915A-37	Sequence 37, Appl
36	61.5	41.8	1400	4 US-09-879-957-37	Sequence 7, Appl
37	61	41.5	17	1 US-08-322-962-7	Sequence 7, Appl
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39	61	41.5	75	1 US-08-322-962-5	Sequence 5, Appl
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44	60.5	41.2	24	1 US-08-249-322A-41	Sequence 41, Appl
45	60.5	41.2	24	1 US-08-469-566A-41	Sequence 41, Appl

RESULT 1
US-09-948-495A-4
; Sequence 4, Application US/09948495A
; Patent No. 6750036
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated
; FILE REFERENCE: 21089-11
; CURRENT APPLICATION NUMBER: US/09/948,495A
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Fastseq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artemia
US-09-948-495A-4

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Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDCKDGTCTCAPDCKCAKDCKC 22
Db 1 MDCKDGTCTCAPDCKCAKDCKC 22

RESULT 2
US-09-948-495A-2
; Sequence 2, Application US/09948495A
; Patent No. 6750056
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated
; FILE REFERENCE: 21089-11
; CURRENT APPLICATION NUMBER: US/09/948,495A
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 48
; TYPE: PAT
; ORGANISM: Artemia
US-09-948-495A-2

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDCKDGTCTCAPDCKCAKDCKC 22

Search completed: December 20, 2004, 14:54:17
Job time : 18.2857 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 20, 2004, 14:52:40 ; Search time 62.8571 Seconds
(without alignments)
125.242 Million cell updates/sec

Title: US-10-797-748-4
Perfect score: 147
Sequence: 1 MDCKDGTCTCAPDCKCAKDCKC 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID
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8	74	50.3	2837	14	US-10-142-885-229
9	74	50.3	2837	14	US-10-158-790-229
10	74	50.3	2837	14	US-10-137-871-229
11	74	50.3	2837	14	US-10-140-923-229
12	74	50.3	2837	14	US-10-141-756-229
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ALIGNMENTS

RESULT 1
US-09-948-495A-4
; Sequence 4, Application US/09948495A
; Publication No. US20030105304A1

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? GENERAL INFORMATION:
? APPLICANT: Acey, Roger A.
? TITLE OF INVENTION: Metal Binding Proteins and Associated
? TITLE OF INVENTION: Methods
? FILE REFERENCE: 21089-11
? CURRENT APPLICATION NUMBER: US/09/948,495A
? CURRENT FILING DATE: 2001-09-06
? NUMBER OF SEQ ID NOS: 10
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 4
? LENGTH: 22
? TYPE: PRT
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; Publication No. US20030105304A1
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 21089-11
; CURRENT APPLICATION NUMBER: US/09/948.495A
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: Artemia
US-09-948-495A-2

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OM protein - protein search, using sw model

Run on: December 20, 2004, 14:46:34 ; Search time 207.743 Seconds
(without alignments)
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Title: US-10-797-748-4
Perfect score: 147
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Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	22	33	US-10-797-748-4
2	147	100.0	48	33	US-10-797-748-2
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4	86	58.5	64	30	US-10-425-115-264601
5	81	55.1	64	22	US-09-791-537-138368
6	77	52.4	26	26	US-10-030-019A-258
7	76.5	52.0	67	1	PCT-US01-04098A-3060
8	76.5	52.0	28	28	US-10-258-899A-3060
9	76.5	52.0	67	28	US-10-293-244-3060
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13	74	50.3	67	22	US-09-791-537-138315
14	74	50.3	1606	36	US-60-592-191-242
15	74	50.3	2837	27	US-10-137-871-229
16	74	50.3	3089	27	US-10-158-790-229
17	74	50.3	3089	27	US-10-176-912-61
18	74	50.3	3089	27	US-10-179-524-61
19	74	50.3	3089	27	US-10-184-634-61
20	74	50.3	3089	27	US-10-184-644-61
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35	73.5	50.0	61	27	US-10-170-205E-29424
36	73.5	50.0	61	27	US-10-170-385-265
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39	73.5	50.0	61	30	US-10-425-115-196037	Sequence 196037,
40	73.5	50.0	61	31	US-10-505-928-668	Sequence 668, App
41	73.5	50.0	61	33	US-10-743-643-11	Sequence 11, Appl
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ALIGNMENTS

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; Sequence 4, Application US/10797748
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated Methods
; FILE REFERENCE: 51302-00002
; CURRENT APPLICATION NUMBER: US/10/797,748
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 09/948,495
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 4
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; TYPE: PR1
; ORGANISM: Artemia sp.
US-10-797-748-4
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 2, Application US/10797748
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated Methods
; FILE REFERENCE: 51302-00002
; CURRENT APPLICATION NUMBER: US/10/797,748
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 09/948,495
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2
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; TYPE: PR1
; ORGANISM: Artemia sp.
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US-10-797-748-2

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDCKDGGCTCAPDCKCAKDKKC 22
Db 1 MDCKDGGCTCAPDCKCAKDKKC 22
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Search completed: December 20, 2004, 15:05:24
Job time : 208.743 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 14:49:24 ; Search time 10.0571 Seconds
(without alignments)
99.072 Million cell updates/sec

Title: US-10-797-748-4

Perfect score: 147
Sequence: 1 MDCKDCTCAPDKCAKDCKC 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169693 seqs, 45290116 residues

Total number of hits satisfying chosen parameters: 169693

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*

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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

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5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

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8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	69.5	47.3	61	1	PCT-US04-36404-184
2	69.5	47.3	62	6	US-10-475-075-254
3	69.5	47.3	78	6	US-10-475-075-265
4	69	46.9	251	6	US-10-732-923-14194
5	68.5	46.6	61	1	PCT-US04-36404-181
6	68.5	46.6	61	6	US-10-872-024-161
7	68.5	46.6	89	6	US-10-220-366A-27761
8	68.5	46.6	90	6	US-10-972-024-453
9	65	44.2	35823	6	US-10-874-049-1

10	63	42.9	199	6	US-10-399-103A-834	Sequence 834, App
11	62.5	42.5	61	1	PCT-US04-36404-183	Sequence 183, App
12	62.5	42.5	61	1	PCT-US04-36404-186	Sequence 186, App
13	62.5	42.5	61	6	US-10-972-024-211	Sequence 211, App
14	62.5	42.5	71	6	US-10-220-366A-27416	Sequence 27416, A
15	62	42.2	35346	6	US-10-874-049-2	Sequence 2, App11
16	61.5	41.8	21	6	US-10-966-673-64	Sequence 64, App1
17	60.5	41.2	24	6	US-10-844-218-41	Sequence 41, App
18	60.5	41.2	1076	6	US-10-955-952-219	Sequence 219, App
19	60.5	41.2	1076	6	US-10-157-779-219	Sequence 219, App
20	60.5	41.2	1076	6	US-10-964-241-219	Sequence 219, App
21	60.5	41.2	1200	1	PCT-US04-36439-18	Sequence 18, App1
22	60	40.8	1602	6	US-10-962-128-4	Sequence 4, App11
23	60	40.5	1200	6	US-10-962-128-4	Sequence 4, App11
24	59.5	40.5	1200	6	US-10-914-735-3	Sequence 3, App11
25	57.5	39.1	327	6	US-10-891-972-110	Sequence 110, App
26	57.5	39.1	327	6	US-10-891-972-112	Sequence 112, App
27	57.5	39.1	327	6	US-10-891-972-114	Sequence 114, App
28	57.5	39.1	327	6	US-10-891-972-116	Sequence 116, App
29	57.5	39.1	327	6	US-10-891-972-118	Sequence 118, App
30	57.5	39.1	327	6	US-10-891-972-120	Sequence 120, App
31	57.5	39.1	327	6	US-10-891-972-122	Sequence 122, App
32	57.5	39.1	327	6	US-10-891-972-124	Sequence 124, App
33	57.5	39.1	327	6	US-10-891-972-126	Sequence 126, App
34	57.5	39.1	327	6	US-10-891-972-128	Sequence 128, App
35	57.5	39.1	327	6	US-10-891-972-130	Sequence 130, App
36	57.5	39.1	327	6	US-10-891-972-132	Sequence 132, App
37	57.5	39.1	514	6	US-10-990-328-8719	Sequence 8719, Ap
38	57	38.8	28	6	US-10-915-740A-1065	Sequence 1065, Ap
39	57	38.8	111	6	US-10-220-366A-15700	Sequence 15700, A
40	56.5	38.4	1140	6	US-10-972-983-2	Sequence 2, App11
41	56.5	38.4	1140	6	US-10-408-765-1838	Sequence 1838, Ap
42	56	38.1	789	6	US-10-874-049-5	Sequence 5, App11
43	56	38.1	900	6	US-10-874-049-7	Sequence 7, App11
44	55	37.4	119	6	US-10-220-366A-1903	Sequence 1903, A
45	54.5	37.1	173	6	US-10-490-147A-6	Sequence 6, App11

Search completed: December 20, 2004, 15:06:02
Job time : 10.0571 secs

ON protein - protein search, using sw model

Run on: December 20, 2004, 14:44:03 ; Search time 37.7143 Seconds
(without alignments)
84,405 Million cell updates/sec

Title: US-10-797-748-2
Perfect score: 320
Sequence: 1 MDCKDCTCAFDCKAKADC.....KSPCEKCEKDCSCSCGH 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:
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4: /cgn2_6/ptodate/1/1aa/6B_CONB.pep:.*
5: /cgn2_6/ptodate/1/1aa/6C_CONB.pep:.*
6: /cgn2_6/ptodate/1/1aa/6D_CONB.pep:.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	320	100.0	48	4	US-09-948-495A-2
2	147	45.9	22	4	US-09-948-495A-4
3	117	36.6	1417	3	US-08-900-230-3
4	114.5	35.8	1400	3	US-08-630-915A-37
5	114.5	35.8	1400	4	US-09-879-957-37
6	110.5	34.5	68	1	US-07-696-051B-1
7	110.5	34.5	68	1	US-07-924-063A-1
8	110.5	34.5	68	1	US-08-138-340B-2
9	109.5	34.2	61	4	US-09-919-039-31
10	109.5	34.2	254	2	US-08-767-026-7
11	109.5	34.2	254	4	US-09-319-275A-7

12	109	34.1	2088	4	US-09-548-372D-13	Sequence 13, Appl
13	109	34.1	2088	4	US-09-548-367D-13	Sequence 19, Appl
14	109	34.1	2088	4	US-09-551-853D-13	Sequence 11, Appl
15	109	34.1	2088	4	US-09-548-376D-13	Sequence 13, Appl
16	109	34.1	2088	4	US-09-548-373D-13	Sequence 13, Appl
17	109	34.1	2088	4	US-09-548-366F-13	Sequence 13, Appl
18	107	33.4	2732	4	US-09-086-436-30	Sequence 30, Appl
19	105.5	33.0	62	3	US-07-780-717C-5	Sequence 5, Appl
20	105	32.8	1497	4	US-09-060-854B-2	Sequence 3, Appl
21	104.5	32.7	61	2	US-08-785-530-3	Sequence 3, Appl
22	104.5	32.7	61	2	US-09-123-850-3	Sequence 19, App
23	104.5	32.7	61	4	US-09-919-039-195	Sequence 1, Appl
24	104.5	32.7	2211	3	US-09-738-884-1	Sequence 1, Appl
25	104.5	32.7	2211	4	US-10-096-961A-1	Sequence 5, Appl
26	103.5	32.3	75	1	US-08-322-962-5	Sequence 5, Appl
27	103.5	32.3	75	3	US-08-450-653-5	Sequence 6, Appl
28	103	32.2	61	2	US-08-785-530-6	Sequence 6, Appl
29	103	32.2	61	2	US-09-123-850-6	Sequence 6, Appl
30	102.5	32.0	61	2	US-08-785-530-5	Sequence 5, Appl
31	102.5	32.0	61	2	US-09-123-850-5	Sequence 5, Appl
32	102.5	32.0	1917	4	US-09-627-650B-5	Sequence 5, Appl
33	102.5	32.0	1917	4	US-09-436-063C-5	Sequence 4, Appl
34	102	31.9	61	2	US-08-785-530-4	Sequence 4, Appl
35	102	31.9	61	2	US-09-123-850-4	Sequence 4, Appl
36	99.5	31.1	61	4	US-09-919-039-272	Sequence 212, App
37	98.5	30.8	61	4	US-09-919-039-245	Sequence 212, App
38	98.5	30.8	82	4	US-09-270-767-32606	Sequence 34606, A
39	98.5	30.8	82	4	US-09-270-767-47823	Sequence 22, Appl
40	98	30.6	120	3	US-08-508-761B-22	Sequence 44, Appl
41	96.5	30.2	908	4	US-08-714-761-44	Sequence 3, Appl
42	96.5	30.2	1345	2	US-08-977-767-3	Sequence 7, Appl
43	94.5	29.5	2508	4	US-09-627-650B-7	Sequence 7, Appl
44	94.5	29.5	2508	4	US-09-436-063C-7	Sequence 3, Appl
45	94.5	29.5	2544	4	US-09-627-650B-3	

ALIGNMENTS

RESULT 1
US-09-948-495A-2
; Sequence 2, Application US/09948495A
; Patent No. 6750056
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated
; FILE REFERENCE: 21089-11
; CURRENT APPLICATION NUMBER: US/09/948, 495A
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artemia
US-09-948-495A-2

Query Match 100.0%; Score 320; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 9.1e-20;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

Qy 1 MDCCKDGTCAPDCKAKDKCKGCECKSDPECKECDCSCGCH 48
Db 1 MDCCKDGTCAPDCKAKDKCKGCECKSDPECKECDCSCGCH 48

RESULT 2

US-09-948-495A-4
; Sequence 4, Application US/09948495A
; Patent No. 6750056
; GENERAL INFORMATION:
; APPLICANT: Acay, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated
; FILE REFERENCE: 21089-11
; CURRENT APPLICATION NUMBER: US/09/948,495A
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ. ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ. ID NO. 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artemia
US-09-948-495A-4

Query Match 45.9%; Score 147; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDCCKDGTCAPDCKAKDKCK 22
Db 1 MDCCKDGTCAPDCKAKDKCK 22

Search completed: December 20, 2004, 14:54:16
Job time : 39.7143 secs

OM protein - protein search, using sw model

Run on: December 20, 2004, 14:52:40 ; Search time 137.143 Seconds
(without alignments)
125.242 Million cell updates/sec

Title: US-10-797-748-2
Perfect score: 320
Sequence: 1 MDCCKDGTCAPDCKAKDKC.....KSDPECKECDCSCGCH 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Match	Length	DB	ID	Description
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4	125	39.1	4185	14	US-10-146-731-67	Sequence 67, Appl
5	125	39.1	4185	14	US-10-140-472-67	Sequence 67, Appl
6	125	39.1	4185	14	US-10-141-761-67	Sequence 67, Appl
7	125	39.1	4185	14	US-10-142-885-67	Sequence 67, Appl
8	125	39.1	4185	14	US-10-158-790-67	Sequence 67, Appl
9	125	39.1	4185	14	US-10-137-871-67	Sequence 67, Appl
10	125	39.1	4185	14	US-10-140-923-67	Sequence 67, Appl
11	125	39.1	4185	14	US-10-141-756-67	Sequence 67, Appl
12	125	39.1	4185	14	US-10-141-759-67	Sequence 67, Appl
13	125	39.1	4185	14	US-10-140-805-67	Sequence 67, Appl
14	125	39.1	4185	14	US-10-140-864-67	Sequence 67, Appl
15	125	39.1	4185	15	US-10-142-426-67	Sequence 67, Appl
16	119.5	37.3	1523	14	US-10-123-155-429	Sequence 429, App
17	119.5	37.3	1523	14	US-10-146-731-429	Sequence 429, App
18	119.5	37.3	1523	14	US-10-140-472-429	Sequence 429, App
19	119.5	37.3	1523	14	US-10-141-761-429	Sequence 429, App
20	119.5	37.3	1523	14	US-10-142-885-429	Sequence 429, App
21	119.5	37.3	1523	14	US-10-158-790-429	Sequence 429, App
22	119.5	37.3	1523	14	US-10-137-871-429	Sequence 429, App
23	119.5	37.3	1523	14	US-10-140-923-429	Sequence 429, App
24	119.5	37.3	1523	14	US-10-141-756-429	Sequence 429, App
25	119.5	37.3	1523	14	US-10-141-759-429	Sequence 429, App
26	119.5	37.3	1523	14	US-10-140-805-429	Sequence 429, App
27	119.5	37.3	1523	14	US-10-140-864-429	Sequence 429, App
28	119.5	37.3	1523	15	US-10-142-426-429	Sequence 429, App
29	119	37.2	371	16	US-10-437-963-146358	Sequence 146358,
30	118	36.9	2276	14	US-10-123-155-9	Sequence 9, Appl
31	118	36.9	2276	14	US-10-146-731-9	Sequence 9, Appl
32	118	36.9	2276	14	US-10-140-472-9	Sequence 9, Appl
33	118	36.9	2276	14	US-10-141-761-9	Sequence 9, Appl
34	118	36.9	2276	14	US-10-142-885-9	Sequence 9, Appl
35	118	36.9	2276	14	US-10-158-790-9	Sequence 9, Appl
36	118	36.9	2276	14	US-10-137-871-9	Sequence 9, Appl
37	118	36.9	2276	14	US-10-140-923-9	Sequence 9, Appl
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39	118	36.9	2276	14	US-10-141-759-9	Sequence 9, Appl
40	118	36.9	2276	14	US-10-140-805-9	Sequence 9, Appl
41	118	36.9	2276	14	US-10-140-864-9	Sequence 9, Appl
42	118	36.9	2276	15	US-10-142-426-9	Sequence 9, Appl
43	117	36.6	75	17	US-10-425-115-339798	Sequence 339798,
44	117	36.6	1417	8	US-08-900-230-3	Sequence 3, Appl
45	116.5	36.4	1536	14	US-10-184-644-461	Sequence 461, App

ALIGNMENTS

RESULT 1
 US-09-948-495A-2
 ; Sequence 2, Application US/09948495A
 ; Publication No. US20030105304A1

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; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated
; FILE OF INVENTION: Methods
; FILE REFERENCE: 21089-11
; CURRENT APPLICATION NUMBER: US/09/948,495A
; CURRENT FILING DATE: 2001-09-06
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artemia
US-09-948-495A-2

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Query Match          100.0%; Score 320; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
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Db       1 MDCKDGTCTCAPDKCKADCKCKGCECKSDPECKCKDCSCDCSCGCH 48

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RESULT 2
US-09-948-495A-4
; Sequence 4, Application US/09948495A
; Publication No. US20030105304A1
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated
; FILE OF INVENTION: Methods
; FILE REFERENCE: 21089-11
; CURRENT APPLICATION NUMBER: US/09/948,495A
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artemia
US-09-948-495A-4

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Query Match          45.9%; Score 147; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db       1 MDCKDGTCTCAPDKCKADCKCK 22

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Search completed: December 20, 2004, 15:09:29
 Job time : 139.143 secs

OM protein - protein search, using sw model

Run on: December 20, 2004, 14:46:34 ; Search time 453.257 Seconds
(without alignments)
117.337 Million cell1 updates/sec

Title: US-10-797-748-2
Perfect score: 320
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/pae/US0105_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	147	45.9	22	33 US-10-797-748-4	Sequence 4, Appl1
3	136	42.5	201	18 US-09-417-507-40083	Sequence 40083, A
4	135.5	42.3	69	26 US-10-030-019A-258	Sequence 258, App
5	125	39.1	124	22 US-09-791-537-90183	Sequence 90183, A
6	125	39.1	4185	27 US-10-137-871-67	Sequence 67, Appl
7	125	39.1	4185	27 US-10-137-871-67	Sequence 67, Appl
8	124	38.8	66	22 US-09-791-537-44042	Sequence 150823, A
9	121	37.8	73	22 US-09-791-537-139183	Sequence 44042, A
10	119.5	37.3	73	22 US-09-791-537-139837	Sequence 139183, A
11	119.5	37.3	73	22 US-10-137-871-429	Sequence 139837, A
12	119.5	37.3	1523	27 US-10-137-871-429	Sequence 429, App
13	119.5	37.3	1523	27 US-10-137-871-429	Sequence 429, App
14	119	37.2	371	30 US-10-437-963-146358	Sequence 146358, A
15	119	37.2	426	30 US-10-449-902-54143	Sequence 54143, A
16	119	37.2	645	1 PCT-US03-26780-3122	Sequence 3122, App
17	119	37.2	645	1 PCT-US03-26780-3122	Sequence 3122, App
18	118.5	37.0	73	22 US-09-791-537-152253	Sequence 152253, A
19	118.5	37.0	9090	36 US-60-592-191-169	Sequence 169, App
20	118.5	37.0	9091	36 US-60-592-191-170	Sequence 170, App
21	118	36.9	2276	27 US-10-137-871-9	Sequence 9, Appl1
22	118	36.9	2276	27 US-10-158-790-9	Sequence 9, Appl1
23	117.5	36.7	1470	1 PCT-US03-26780-3288	Sequence 3288, App
24	117	36.6	75	30 US-10-425-115-339798	Sequence 339798, A
25	116.5	36.4	1536	27 US-10-176-912-461	Sequence 461, App
26	116.5	36.4	1536	27 US-10-176-912-461	Sequence 461, App
27	116.5	36.4	1536	27 US-10-184-634-461	Sequence 461, App
28	116.5	36.4	1536	27 US-10-184-644-461	Sequence 461, App
29	116	36.2	82	30 US-10-425-115-274137	Sequence 274137, A
30	116	36.2	82	33 US-10-767-701-47286	Sequence 47286, A
31	116	36.2	83	33 US-10-767-701-51725	Sequence 51725, A
32	115.5	36.1	58	22 US-09-791-537-44062	Sequence 44062, A
33	115.5	36.1	73	22 US-09-791-537-90123	Sequence 90123, A
34	115.5	36.1	375	1 PCT-US03-26780-2604	Sequence 2604, App
35	115.5	36.1	1524	27 US-10-176-912-421	Sequence 421, App
36	115.5	36.1	1524	27 US-10-176-912-421	Sequence 421, App
37	115.5	36.1	1524	27 US-10-184-634-421	Sequence 421, App
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39	115.5	36.1	2572	1	PCT-US01-12836-26	Sequence 26, Appl
40	115.5	36.1	2572	19	US-09-559-001-26	Sequence 26, Appl
41	115.5	36.1	2572	21	US-09-728-403-26	Sequence 26, Appl
42	115.5	36.1	2572	21	US-09-728-403-26	Sequence 26, Appl
43	115.5	36.1	3236	27	US-10-137-871-369	Sequence 369, App
44	115.5	36.1	3296	27	US-10-138-790-369	Sequence 369, App
45	115	35.9	2934	1	PCT-US03-26780-2987	Sequence 2987, Ap

ALIGNMENTS

RESULT 1
US-10-797-748-2
; Sequence 2, Application US/10797748
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated Methods
; FILE REFERENCE: 51302-00002
; CURRENT APPLICATION NUMBER: US/10/797,748
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 09/948,495
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artemia sp.
US-10-797-748-2

Query Match 100.0%; Score 320; DB 33; Length 48;
Best Local Similarity 100.0%; Pred. No. 3e-20;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-797-748-4
; Sequence 4, Application US/10797748
; GENERAL INFORMATION:
; APPLICANT: Acey, Roger A.
; TITLE OF INVENTION: Metal Binding Proteins and Associated Methods
; FILE REFERENCE: 51302-00002
; CURRENT APPLICATION NUMBER: US/10/797,748
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 09/948,495
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artemia sp.

US-10-797-748-4

Query Match 45.9%; Score 147; DB 33; Length 22;
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OM protein - protein search, using SW model

Run on: December 20, 2004, 14:49:24 ; Search time 21.9429 Seconds
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Title: US-10-797-748-2

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Searched: 169693 seqs, 45290116 residues

Total number of hits satisfying chosen parameters: 169693

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	102.5	32.0	62	6	US-10-475-075-254
5	101.5	31.7	61	1	PCT-US04-36404-184
6	99.5	31.1	61	1	PCT-US04-36404-181
7	99.5	31.1	61	6	US-10-972-024-161
8	99.3	31.1	89	6	US-10-220-366A-27761
9	99	30.9	900	6	US-10-874-049-7

10	98.5	30.8	61	1	PCT-US04-36404-186	Sequence 186, App
11	98.5	30.8	61	6	US-10-972-024-211	Sequence 211, App
12	98.5	30.8	71	6	US-10-220-366A-27416	Sequence 27416, A
13	98.5	30.8	90	6	US-10-972-024-453	Sequence 453, App
14	98.5	30.8	35346	6	US-10-874-049-2	Sequence 2, App11
15	97.5	30.5	1602	1	PCT-US04-33017-4	Sequence 4, App11
16	97.5	30.5	1602	6	US-10-962-128-4	Sequence 834, App
17	97	30.3	199	6	US-10-399-103A-834	Sequence 1874, Ap
18	94	29.4	62	6	US-10-408-765-1874	Sequence 183, App
19	93.5	29.2	61	1	PCT-US04-36404-183	Sequence 219, App
20	93.5	29.2	1076	6	US-10-955-952-219	Sequence 219, App
21	93.5	29.2	1076	6	US-10-157-779-219	Sequence 219, App
22	93.5	29.2	1076	6	US-10-964-241-219	Sequence 3, App11
23	93	29.1	786	6	US-10-874-049-3	Sequence 3, App11
24	93	29.1	1200	6	US-10-914-735-3	Sequence 27094, A
25	92.5	28.9	129	6	US-10-220-366A-27094	Sequence 3, App11
26	92.5	28.9	2055	6	US-10-481-582-3	Sequence 16365, A
27	92.5	28.9	2497	6	US-10-481-582-4	Sequence 110, App
28	92	28.7	127	6	US-10-220-366A-16365	Sequence 112, App
29	91	28.4	71	6	US-10-985-299-32	Sequence 114, App
30	90	28.1	327	6	US-10-891-972-110	Sequence 116, App
31	90	28.1	327	6	US-10-891-972-112	Sequence 118, App
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33	90	28.1	327	6	US-10-891-972-116	Sequence 122, App
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39	90	28.1	327	6	US-10-891-972-128	Sequence 134, App
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41	90	28.1	327	6	US-10-891-972-132	Sequence 138, App
42	88.5	27.7	119	6	US-10-220-366A-14903	Sequence 139, App
43	87.5	27.3	366	6	US-10-990-328-10412	Sequence 140, App
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